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1600

RAW SEQUENCE LISTING

DATE: 02/10/2003

PATENT APPLICATION: US/09/512,581B

TIME: 15:10:37

Input Set : A:\seqlistcorrected3.txt

Output Set: N:\CRF4\02102003\I512581B.raw

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3 <110> APPLICANT: Soto, Ana M.
4   Sonnenschein, Carlos
5   Geck, Peter
6   Szelei, Jozsef
8 <120> TITLE OF INVENTION: A NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL
9   PROLIFERATION AND USES THEREOF
11 <130> FILE REFERENCE: MBI-008
13 <140> CURRENT APPLICATION NUMBER: US 09/512,581B
14 <141> CURRENT FILING DATE: 2000-02-24
16 <150> PRIOR APPLICATION NUMBER: US 60/121,461
17 <151> PRIOR FILING DATE: 1999-02-24
19 <160> NUMBER OF SEQ ID NOS: 8
21 <170> SOFTWARE: PatentIn Ver. 2.0
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26 <213> ORGANISM: Homo sapiens
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36   Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr
37       1           5           10           15
39 ccg cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg 158
40 Pro Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met
41           20           25           30
43 gtg aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag 206
44 Val Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln
45           35           40           45
47 gac tct gaa gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt 254
48 Asp Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu
49           50           55           60
51 gct tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta ctg 302
52 Ala Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu
53           65           70           75
55 gta gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct 350
56 Val Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala
57   80           85           90           95
59 cct tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca 398
60 Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr
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63 aga cag ttg aag ggg cta gag gat aca aag agc cca caa ttc aat agg 446
64 Arg Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg
65      115      120      125
67 tat ttt tat tta ctt gag aac att gct tgg gtc aag tca tat aac ata 494
68 Tyr Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile
69      130      135      140
71 tgc ttt gag tta gaa gat agc aat gaa att ttc acc cag cta tac aga 542
72 Cys Phe Glu Leu Glu Asp Ser Asn Glu Ile Phe Thr Gln Leu Tyr Arg
73      145      150      155
75 acc tta ttt tca gtt ata aac aat ggc cac aat cag aaa gtc cat atg 590
76 Thr Leu Phe Ser Val Ile Asn Asn Gly His Asn Gln Lys Val His Met
77 160      165      170      175
79 cac atg gta gac ctt atg agc tct att att tgt gaa ggt gat aca gtg 638
80 His Met Val Asp Leu Met Ser Ser Ile Ile Cys Glu Gly Asp Thr Val
81      180      185      190
83 tct cag gag ctt ttg gat acg gtt tta gta aat ctg gta cct gct cat 686
84 Ser Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His
85      195      200      205
87 aag aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag 734
88 Lys Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys
89      210      215      220
91 agg aca gct caa gct att gag cca tat att acc act ttt ttt aat cag 782
92 Arg Thr Ala Gln Ala Ile Glu Pro Tyr Ile Thr Thr Phe Phe Asn Gln
93      225      230      235
95 gtt ctg atg ctt ggg aaa aca tct atc agc gat ttg tca gag cat gtc 830
96 Val Leu Met Leu Gly Lys Thr Ser Ile Ser Asp Leu Ser Glu His Val
97 240      245      250      255
99 ttt gac tta att ttg gag ctc tac aat att gat agt cat ttg ctg ctc 878
100 Phe Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu
101      260      265      270
103 tct gtt tta ccc cag ctt gaa ttt aaa tta aag agc aat gat aat gag 926
104 Ser Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu
105      275      280      285
107 gag cgc cta caa gtt gtt aaa cta ctg gca aaa atg ttt ggg gca aag 974
108 Glu Arg Leu Gln Val Val Lys Leu Leu Ala Lys Met Phe Gly Ala Lys
109      290      295      300
111 gat tca gaa ttg gct tct caa aac aag cca ctt tgg cag tgc tac ttg 1022
112 Asp Ser Glu Leu Ala Ser Gln Asn Lys Pro Leu Trp Gln Cys Tyr Leu
113      305      310      315
115 ggc agg ttt aat gat atc cat gta cca atc cgc ctg gaa tgt gtg aaa 1070
116 Gly Arg Phe Asn Asp Ile His Val Pro Ile Arg Leu Glu Cys Val Lys
117 320      325      330      335
119 ttt gct agc cat tgt ctc atg aac cat cct gat tta gca aaa gac tta 1118
120 Phe Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu
121      340      345      350
123 aca gag tat ctt aaa gtg agg tca cat gac cct gag gaa gct att aga 1166
124 Thr Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg
125      355      360      365
127 cat gat gtt att gtg tca ata gtt aca gct gct aaa aag gat att ctt 1214

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128 His Asp Val Ile Val Ser Ile Val Thr Ala Ala Lys Lys Asp Ile Leu
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131 ctg gtc aat gat cac tta ctt aat ttt gtg aga gag aga aca tta gac 1262
132 Leu Val Asn Asp His Leu Leu Asn Phe Val Arg Glu Arg Thr Leu Asp
133          385          390          395
135 aaa cga tgg aga gta cgc aaa gaa gcc atg atg gga ctt gcc caa att 1310
136 Lys Arg Trp Arg Val Arg Lys Glu Ala Met Met Gly Leu Ala Gln Ile
137 400          405          410          415
139 tat aag aaa tat gct tta cag tca gca gct gga aaa gat gct gca aaa 1358
140 Tyr Lys Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys
141          420          425          430
143 cag ata gca tgg atc aaa gac aaa ttg cta cat ata tat tat caa aat 1406
144 Gln Ile Ala Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn
145          435          440          445
147 agt att gat gat cga cta ctt gtt gaa cgg atc ttt gct caa tac atg 1454
148 Ser Ile Asp Asp Arg Leu Leu Val Glu Arg Ile Phe Ala Gln Tyr Met
149          450          455          460
151 gtt cct cac aat tta gaa act aca gaa cgg atg aaa tgc tta tat tac 1502
152 Val Pro His Asn Leu Glu Thr Thr Glu Arg Met Lys Cys Leu Tyr Tyr
153          465          470          475
155 ttg tat gcc aca ctg gat tta aat gct gtg aaa gca ttg aat gaa atg 1550
156 Leu Tyr Ala Thr Leu Asp Leu Asn Ala Val Lys Ala Leu Asn Glu Met
157 480          485          490          495
159 tgg aaa tgt caa aat ctg ctc cga cat caa gta aag gat ttg ctt gac 1598
160 Trp Lys Cys Gln Asn Leu Leu Arg His Gln Val Lys Asp Leu Leu Asp
161          500          505          510
163 ttg att aag caa ccc aaa aca gat gcc agt gtc aag gcc ata ttt tca 1646
164 Leu Ile Lys Gln Pro Lys Thr Asp Ala Ser Val Lys Ala Ile Phe Ser
165          515          520          525
167 aaa gtg atg gtt att aca aga aat tta cct gat cct ggt aag gct cag 1694
168 Lys Val Met Val Ile Thr Arg Asn Leu Pro Asp Pro Gly Lys Ala Gln
169          530          535          540
171 gat ttc atg aag aaa ttc aca cag gtg tta gaa gat gat gag aaa ata 1742
172 Asp Phe Met Lys Lys Phe Thr Gln Val Leu Glu Asp Asp Glu Lys Ile
173          545          550          555
175 aga aag cag tta gaa gta ctt gtt agt cca aca tgc tcc tgc aag cag 1790
176 Arg Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln
177 560          565          570          575
179 gct gaa ggt tgt gtg cgt gaa ata act aag aag ttg ggc aac ccc aaa 1838
180 Ala Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys
181          580          585          590
183 cag cct aca aat cct ttc ctg gaa atg atc aag ttt ctc ttg gag agg 1886
184 Gln Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg
185          595          600          605
187 ata gca cct gtg cac ata gat acc gaa tct atc agt gct ctt att aaa 1934
188 Ile Ala Pro Val His Ile Asp Thr Glu Ser Ile Ser Ala Leu Ile Lys
189          610          615          620
191 caa gtg aac aaa tca ata gat gga aca gca gat gat gaa gat gag ggt 1982
192 Gln Val Asn Lys Ser Ile Asp Gly Thr Ala Asp Asp Glu Asp Glu Gly

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193	625	630	635	
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196	Val Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val			
197	640	645	650	655
199	ctc tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa	2078		
200	Leu Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu			
201	660	665	670	
203	tca tta ctg gct tgt ctg aaa atg gat gat gaa aaa gta gca gaa gct	2126		
204	Ser Leu Leu Ala Cys Leu Lys Met Asp Glu Lys Val Ala Glu Ala			
205	675	680	685	
207	gca cta caa att ttc aaa aac aca gga agc aaa att gaa gag gat ttt	2174		
208	Ala Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe			
209	690	695	700	
211	cca cac atc aga tca gcc ttg ctt cct gtt tta cat cac aaa tct aaa	2222		
212	Pro His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys			
213	705	710	715	
215	aaa gga ccc ccc cgt caa gcc aaa tat gcc att cat tgt atc cat gcg	2270		
216	Lys Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala			
217	720	725	730	735
219	ata ttt tct agt aaa gag acc cag ttt gca cag ata ttt gag cct ctg	2318		
220	Ile Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu			
221	740	745	750	
223	cat aag agc cta gat cca agc aac ctg gaa cat ctc ata aca cca ttg	2366		
224	His Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu			
225	755	760	765	
227	ggt act att ggt cat att gct ctc ctt gca cct gat caa ttt gct gct	2414		
228	Val Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala			
229	770	775	780	
231	cct tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg	2462		
232	Pro Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met			
233	785	790	795	
235	aat gat cgg ctt cca ggg aaa aag aca act aaa ctt tgg gtt cca gat	2510		
236	Asn Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp			
237	800	805	810	815
239	gaa gaa gta tct cct gag aca atg gtc aaa att cag gct att aaa atg	2558		
240	Glu Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met			
241	820	825	830	
243	atg gtt cga tgg cta ctt gga atg aaa aat aat cac agt aaa tca gga	2606		
244	Met Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly			
245	835	840	845	
247	act tct acc tta aga ttg cta aca aca ata ttg cat agt gat gga gac	2654		
248	Thr Ser Thr Leu Arg Leu Leu Thr Thr Ile Leu His Ser Asp Gly Asp			
249	850	855	860	
251	ttg aca gaa cag ggg aaa att agt aaa cca gat atg tca cgt ctg aga	2702		
252	Leu Thr Glu Gln Gly Lys Ile Ser Lys Pro Asp Met Ser Arg Leu Arg			
253	865	870	875	
255	ctt gct gct ggg agt gct att gtg aag ctg gca caa gaa ccc tgt tac	2750		
256	Leu Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr			
257	880	885	890	895

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259 cat gaa atc atc aca tta gaa caa tat cag cta tgt gca tta gct atc 2798
260 His Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile
261          900          905          910
263 aac gat gaa tgc tat caa gta aga caa gtg ttt gcc cag aaa ctt cac 2846
264 Asn Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His
265          915          920          925
267 aaa ggc ctt tcc cgt tta cgg ctt cca ctt gag tat atg gca atc tgt 2894
268 Lys Gly Leu Ser Arg Leu Arg Leu Pro Leu Glu Tyr Met Ala Ile Cys
269          930          935          940
271 gcc ctt tgt gca aaa gat cct gta aag gag aga aga gct cat gct agg 2942
272 Ala Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg
273          945          950          955
275 caa tgt ttg gtg aaa aat ata aat gta agg cgg gag tat ctg aag cag 2990
276 Gln Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln
277 960          965          970          975
279 cat gca gct gtt agt gaa aaa tta ttg tct ctt cta cca gag tat gtt 3038
280 His Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val
281          980          985          990
283 gtt cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa 3086
284 Val Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys
285          995          1000          1005
287 gta cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt 3134
288 Val Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe
289          1010          1015          1020
291 gtt ctg gaa ata tta atg gct aaa aat gaa aat aac agt cac gct ttt 3182
292 Val Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe
293          1025          1030          1035
295 atc aga aag atg gta gaa aat att aaa caa aca aaa gat gcc caa gga 3230
296 Ile Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly
297 1040          1045          1050          1055
299 cca gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt 3278
300 Pro Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val
301          1060          1065          1070
303 gcc atg aat atc atc atg tca aag agt act aca tac agt ttg gaa tct 3326
304 Ala Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser
305          1075          1080          1085
307 cct aaa gac ccg gta cta cca gct cgt ttc ttc act caa cct gac aag 3374
308 Pro Lys Asp Pro Val Leu Pro Ala Arg Phe Phe Thr Gln Pro Asp Lys
309          1090          1095          1100
311 aat ttc agt aac acc aaa aat tat ctg cct cct gaa atg aaa tca ttt 3422
312 Asn Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe
313          1105          1110          1115
315 ttc act cct gga aaa cct aaa aca acc aat gtt cta gga gct gtt aac 3470
316 Phe Thr Pro Gly Lys Pro Lys Thr Thr Asn Val Leu Gly Ala Val Asn
317 1120          1125          1130          1135
319 aag cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga 3518
320 Lys Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg
321          1140          1145          1150
323 atg gaa act gta agc aat gca agc agc agc tca aat cca agc tct cct 3566

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Input Set : A:\seqlistcorrected3.txt

Output Set: N:\CRF4\02102003\I512581B.raw

L:1838 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7